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EXAMINER	
RIGGS II, LARRY D	

ART UNIT	PAPER NUMBER
1631	

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Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

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Office Action Summary	Application No.	Applicant(s)	
	10/569,494	TOTIBA ET AL.	
	Examiner	Art Unit	
	LARRY D. RIGGS II	1631	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE *3* MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *05 December 2008*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-13,15 and 16* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-13, 15 and 16* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date _____.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application
6) ☐ Other: _____.

DETAILED ACTION

Applicant's amendments filed 05 December 2008 are acknowledged and entered.

Status of Claims

Claim 14 is cancelled. Claims 1-13, 15 and 16 are currently pending and under consideration.

Drawings

The replacement drawings filed on 05 December 2008 are received and accepted.

Withdrawn Rejections/Objections

The objection of the disclosure in the Office action mailed 05 September 2008 is withdrawn in view of the amendments filed 05 December 2008.

The objection of drawings 3-6, 9 and 11 in the Office action mailed 05 September 2008 is withdrawn in view of the replacement drawings filed 05 December 2008.

The rejection of claims 4, 6, 7, 13 and 14 under 35 U.S.C. 112, Second Paragraph, in the Office action mailed 05 September 2008 is withdrawn in view of the amendments filed 05 December 2008.

The rejection of claims 14 and 15 under 35 U.S.C. 101, in the Office action mailed 05 September 2008 is withdrawn in view of the amendments filed 05 December 2008.

Claim Rejections - 35 USC § 101

35 U.S.C. 101 reads as follows:

> Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

Claims 1-13, 15 and 16 are rejected under 35 U.S.C. 101 because the claimed invention is directed to non-statutory subject matter.

The recent en banc decision regarding Bilski v. Warsaw (2008) set forth that a process is patent-eligible if (1) it is ties to a particular machine or apparatus or (2) it transforms a particular article into a different state or thing.

The instant claims are drawn to a method for visualizing correlation data concerning two biological events or correlation and feature data in a matrix format as well as a general computer program product containing a program to said method. The instant claims are drawn to the abstract process steps of acquiring correlation and feature data, processing the correlation and feature data, and displaying the correlation and feature data.

The instant claims do not recite or inherently involve any transformation of an article, therefore the Examiner must determine if the instant claims have a tie to a particular machine or apparatus. Instant claims 1-13 do not recite any limitation that ties the recited abstract process to any particular machine or apparatus. Further, claims 15 and 15 only recite a computer readable medium comprising executable instructions for carrying out said abstract process, and therefore reads on a general apparatus that would preempt the abstract process.

Further, displaying said interval scores is an insignificant post-solution activity. Nominal or token recitations will not suffice, E.g. displaying, inputting, obtaining, See Ex parte Langemyr (May 28, 2008). Applicants are cautioned against introduction of new matter in an amendment.

For these reasons, claims 1-13, 15 and 16 are considered non-statutory subject matter.

Claim Rejections - 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

The factual inquiries set forth in *Graham* **v.** *John Deere Co.*, 383 U.S. 1, 148 USPQ 459 (1966), that are applied for establishing a background for determining obviousness under 35 U.S.C. 103(a) are summarized as follows:

1. Determining the scope and contents of the prior art.
2. Ascertaining the differences between the prior art and the claims at issue.
3. Resolving the level of ordinary skill in the pertinent art.
4. Considering objective evidence present in the application indicating obviousness or nonobviousness.

This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein

were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

Claims 1-10, 12, 13 and 15 are rejected under 35 U.S.C. 103(a) as being unpatentable over Ge et al. (Nature Genetics, 2001, 29, 482-486) in view of Cushing et al. (US 2005/0010566).

The instant claims provide a method for visualizing correlation data concerning two biological events or the correlation data and feature data regarding each event in a matrix format, the method comprising acquiring and processing correlation and feature data, displaying correlation data concerning biological events of the same or different kinds, or the correlation data and feature data regarding each biological event in (a) one of a plurality of prepared data display formats and at (b) one of a plurality of prepared summarization levels, both of which are selected either manually or automatically depending on the number of data items in desired display data, in order to visualize said correlation and feature data.

Regarding claims 1 and 9, Ge et al. acquired protein-protein pair (feature data) and corresponding genes (correlation data) from three experiments, (page 485, right column, second paragraph) and processed the correlation and feature data, (page 485, right column, last paragraph – page 486). Ge et al. shows a transcriptome-interactome correlation mapping strategy of displaying pair-wise combinations between the clusters

of an expression profiling experiment, with numbers assigned to each cluster in rows and columns of the matrix along with the number of genes each cluster contains in parenthesis, wherein the table on the right shows protein interaction pairs together (feature data) with the expression cluster to which the corresponding genes belong (correlation data), wherein these expression clusters and corresponding genes are displayed simultaneously, (page 482, right column, last paragraph - page 483, left column, first paragraph; Figure 1).

Ge et al. does not show summarization levels.

Cushing et al. shows a summarization level of each row of data, based on rules, that indicates the level of summarization of the data, (paragraphs 155-171).

Regarding claim 2, Ge et al. shows a table of an interaction pair (A), a table of clusters of an expression profiling experiment (B), and a table showing the probability for obtaining at least k observed groups in the intracluster region by chance (C) (Figure 1; Table 1).

Regarding claim 3, Ge et al. shows a two-dimensional matrix by organizing clusters derived from a set of related transcriptional profiling experiments into tow identical axes, wherein pairs of genes whose product can int4eract, according to the clusters to which each gene belongs, (correlation info); For each square, an index of protein interaction density (PID) as the ratio of the number of observed protein interaction pairs to the total number of possible pair-wise combination of protein pairs is calculated (attribute information), (page 483, left column, first paragraph).

Regarding claim 4, Ge et al. shows transcriptome-interactome correlation maps, with calculated protein interaction density (PID) for each square in the matrix as the ratio of interaction of pairs assigned to the square (IP) over the total number of protein pairs possibly formed by combination of the genes in the square (PP) and running diagonally from left to right and indicated by color, (Figure 2).

Regarding claim 5, Ge et al. shows data reduced to a character type (protein interaction pairs) and numeric value type (numbers assigned to each cluster, number of genes each cluster contains, (Figure 1).

Regarding claims 6 and 7, Ge et al. shows character type (protein interaction pairs) and numeric value type (numbers assigned to each cluster, number of genes each cluster contains in a layered structure, a keyword (ORF), rounding values to significant digits and signs or colors indicating ORF pairs, (Figures 1-3, Table 1).

Regarding claim 8, Cushing et al. shows a mechanisms which the results of a multidimensional query are processed such that their format and contents accurately reflect the semantics of an entity/relationship report specification, provides such that the tabular and cross-tabulated reports may be executed using an online analytical programming query, (paragraph 25).

Regarding claim 10, Ge et al. shows protein-protein interactions and clustering analysis data sets of cell cycle-regulated genes, meiosis-regulated genes and cell stress-regulated genes, (page 485, right column, second paragraph). However, it would be obvious that the same display method could be produced with protein-compound interactions, wherein the compounds where of low molecular weight.

Regarding claims 12 and 13, Ge et al. shows that a feature quantity common to members of the cluster are the proteins produced by the genes of the cluster, interact with one another, (abstract, Figure 1). Ge et al. shows a plurality of genes that encode a plurality of interacting proteins wherein these PIDs are expressed in color, (Figures 2-3).

Regarding claim 15, Ge et al. provides a k-means algorithm for clustering analysis with the yeast cell-cycle expression data, (page 483, left column, last paragraph).

Cushing et al. shows a computer readable medium having computer readable code embodied for use in the execution of a method of transforming results of a query into results of a report, (paragraph 14, claim 10).

Regarding claim 16, Ge et al. acquired protein-protein pair (feature data) and corresponding genes (correlation data) from three experiments, (page 485, right column, second paragraph) and processed the correlation and feature data, (page 485, right column, last paragraph – page 486). Ge et al. shows a transcriptome-interactome correlation mapping strategy of displaying pair-wise combinations between the clusters of an expression profiling experiment, with numbers assigned to each cluster in rows and columns of the matrix along with the number of genes each cluster contains in parenthesis, wherein the table on the right shows protein interaction pairs together (feature data) with the expression cluster to which the corresponding genes belong (correlation data), wherein these expression clusters and corresponding genes are displayed simultaneously, (page 482, right column, last paragraph - page 483, left

column, first paragraph; Figure 1). Ge et al. shows a table of an interaction pair (A), a table of clusters of an expression profiling experiment (B), and a table showing the probability for obtaining at least k observed groups in the intracluster region by chance (C) (Figure 1; Table 1). Ge et al. shows that a feature quantity common to members of the cluster are the proteins produced by the genes of the cluster, interact with one another, (abstract, Figure 1). Ge et al. shows a plurality of genes that encode a plurality of interacting proteins wherein these PIDs are expressed in color, (Figures 2-3).

Ge et al. does not show summarization levels.

Cushing et al. shows a summarization level of each row of data, based on rules, that indicates the level of summarization of the data, (paragraphs 155-171).

It would have been obvious to one of ordinary skill in the art at the time of the instant invention to modify the transcriptome-interactome correlation mapping method by Ge et al. with the summarization levels of Cushing et al. because Cushing et al. shows the importance of clustering (grouping) data based on attributes into a hierarchy of levels and aggregating fact values at different levels of summarization, and a person of ordinary skill in the art would understand that visualizing data with the aid of levels of summarization would enable better visualization of the correlation of data, (Cushing et al., paragraph 37). Therefore, one of ordinary skill in the art would recognize the claimed process as a combination of routine applications that are well known the art that and produce no more than expected results.

Claim 10-13, 14, and 15 are rejected under 35 U.S.C. 103(a) as being unpatentable over Ge et al. (Nature Genetics, 2001, 29, 482-486) in view of Cushing et al. (US 2005/0010566) as applied to claims 1-10, 12, 13, 15 and 16 above, and further in view of Artymiuk et al. (J. Mol. Biol., 1994, 243, 327-344).

The instant claim 11 depends from claim 1 with the extra limitation that wherein as the biological events, a structural unit is defined on the basis of atoms in a molecule or a set of atoms in a molecule for each molecule in a complex of one or more molecules, a representative position of the structural unit is defined on the basis of the coordinates of atoms of which the structural unit is composed, and information about the distance between the representative positions of the structural units is displayed in the cells in the matrix, said matrix having each of the structural units as elements in the rows and columns thereof.

Ge et al. and Cushing et al. are applied to claims 1-10, 12, 13, 15 and 16 above. Ge et al. and Cushing et al. do not show a matrix with rows and columns of cells encompassing structural units of molecules, wherein the structural unit are atom(s) in a molecule, with information about distances between structural units.

Artymiuk et al. shows a matrix with rows and columns of cells encompassing structural units of a protein, wherein the structural units are the atoms of amino acids (Histidine 57, Serine 195 and Aspartate 102) encompassing a serine-protease catalytic triad, and providing distances between the respective structural units, (page 331; Figures 2-3).

It would have been obvious to one of ordinary skill in the art at the time of the instant invention to modify the transcriptome-interactome correlation mapping method by Ge et al. with the summarization levels of Cushing et al. and the matrix of structural units with respective distances by Artymiuk et al. because Cushing et al. shows the importance of clustering (grouping) data based on attributes into a hierarchy of levels and aggregating fact values at different levels of summarization, and a person of ordinary skill in the art would understand that visualizing data with the aid of levels of summarization and the aid of matrices with corresponding structural units would enable better visualization of the correlation of data, (Cushing et al., paragraph 37; Artymiuk et al. Figures 2-3 and 6). Therefore, one of ordinary skill in the art would recognize the claimed process as a combination of routine applications that are well known the art that and produce no more than expected results.

Claims 1-10, 12, 13, 15 and 16 are rejected under 35 U.S.C. 103(a) as being unpatentable over Ge et al. (Nature Genetics, 2001, 29, 482-486) in view of Cras et al. (US 2002/0091681).

The instant claims provide a method for visualizing correlation data concerning two biological events or the correlation data and feature data regarding each event in a matrix format, the method comprising acquiring and processing correlation and feature data, displaying correlation data concerning biological events of the same or different kinds, or the correlation data and feature data regarding each biological event in (a) one of a plurality of prepared data display formats and at (b) one of a plurality of prepared

summarization levels, both of which are selected either manually or automatically depending on the number of data items in desired display data, to visualize the correlation and feature data.

Regarding claims 1 and 9, Ge et al. acquired protein-protein pair (feature data) and corresponding genes (correlation data) from three experiments, (page 485, right column, second paragraph) and processed the correlation and feature data, (page 485, right column, last paragraph – page 486). Ge et al. shows a transcriptome-interactome correlation mapping strategy of displaying pair-wise combinations between the clusters of an expression profiling experiment, with numbers assigned to each cluster in rows and columns of the matrix along with the number of genes each cluster contains in parenthesis, wherein the table on the right shows protein interaction pairs together (feature data) with the expression cluster to which the corresponding genes belong (correlation data), wherein these expression clusters and corresponding genes are displayed simultaneously, (page 482, right column, last paragraph - page 483, left column, first paragraph; Figure 1).

Ge et al. does not show summarization levels.

Cras et al. shows a system and method for creating an analytical report on top of a multidimensional data model built on top of a relational or multidimensional database, wherein based on rules or queries a summarization of levels of data may be supplied, (paragraphs 9-13, 48-70, 110-116, 120-121, 129, 174).

Regarding claim 2, Ge et al. shows a table of an interaction pair (A), a table of clusters of an expression profiling experiment (B), and a table showing the probability

for obtaining at least k observed groups in the intracluster region by chance (C) (Figure 1; Table 1).

Regarding claim 3, Ge et al. shows a two-dimensional matrix by organizing clusters derived from a set of related transcriptional profiling experiments into tow identical axes, wherein pairs of genes whose product can int4eract, according to the clusters to which each gene belongs, (correlation info); For each square, an index of protein interaction density (PID) as the ratio of the number of observed protein interaction pairs to the total number of possible pair-wise combination of protein pairs is calculated (attribute information), (page 483, left column, first paragraph).

Regarding claim 4, Ge et al. shows transcriptome-interactome correlation maps, with calculated protein interaction density (PID) for each square in the matrix as the ratio of interaction of pairs assigned to the square (IP) over the total number of protein pairs possibly formed by combination of the genes in the square (PP) and running diagonally from left to right and indicated by color, (Figure 2).

Regarding claim 5, Ge et al. shows data reduced to a character type (protein interaction pairs) and numeric value type (numbers assigned to each cluster, number of genes each cluster contains, (Figure 1).

Regarding claims 6 and 7, Ge et al. shows character type (protein interaction pairs) and numeric value type (numbers assigned to each cluster, number of genes each cluster contains in a layered structure, a keyword (ORF), rounding values to significant digits and signs or colors indicating ORF pairs, (Figures 1-3, Table 1).

Regarding claim 8, Cras et al. shows a mechanisms which the results of a multidimensional query are processed such that their format and contents accurately reflect the semantics of an entity/relationship report specification, such that the tabular and cross-tabulated reports may be executed using an online analytical programming query, (paragraphs 110-116).

Regarding claim 10, Ge et al. shows protein-protein interactions and clustering analysis data sets of cell cycle-regulated genes, meiosis-regulated genes and cell stress-regulated genes, (page 485, right column, second paragraph). However, it would be obvious that the same display method could be produced with protein-compound interactions, wherein the compounds where of low molecular weight.

Regarding claims 12 and 13, Ge et al. shows that a feature quantity common to members of the cluster are the proteins produced by the genes of the cluster, interact with one another, (abstract, Figure 1). Ge et al. shows a plurality of genes that encode a plurality of interacting proteins wherein these PIDs are expressed in color, (Figures 2-3).

Regarding claim 15, Ge et al. provides a k-means algorithm for clustering analysis with the yeast cell-cycle expression data, (page 483, left column, last paragraph).

Cras et al. shows a computer readable medium having computer readable code embodied for use in the execution of a method of transforming results of a query into results of a report, (paragraph 108, claim 13).

Regarding claim 16, Ge et al. acquired protein-protein pair (feature data) and corresponding genes (correlation data) from three experiments, (page 485, right column, second paragraph) and processed the correlation and feature data, (page 485, right column, last paragraph – page 486). Ge et al. shows a transcriptome-interactome correlation mapping strategy of displaying pair-wise combinations between the clusters of an expression profiling experiment, with numbers assigned to each cluster in rows and columns of the matrix along with the number of genes each cluster contains in parenthesis, wherein the table on the right shows protein interaction pairs together (feature data) with the expression cluster to which the corresponding genes belong (correlation data), wherein these expression clusters and corresponding genes are displayed simultaneously, (page 482, right column, last paragraph - page 483, left column, first paragraph; Figure 1). Ge et al. shows a table of an interaction pair (A), a table of clusters of an expression profiling experiment (B), and a table showing the probability for obtaining at least k observed groups in the intracluster region by chance (C) (Figure 1; Table 1). Ge et al. shows that a feature quantity common to members of the cluster are the proteins produced by the genes of the cluster, interact with one another, (abstract, Figure 1). Ge et al. shows a plurality of genes that encode a plurality of interacting proteins wherein these PIDs are expressed in color, (Figures 2-3).

Cras et al. shows a system and method for creating an analytical report on top of a multidimensional data model built on top of a relational or multidimensional database, wherein based on rules or queries a summarization of levels of data may be supplied, (paragraphs 9-13, 48-70, 110-116, 120-121, 129, 174). Cras et al. shows a computer

readable medium having computer readable code embodied for use in the execution of a method of transforming results of a query into results of a report, (paragraph 108, claim 13).

It would have been obvious to one of ordinary skill in the art at the time of the instant invention to modify the transcriptome-interactome correlation mapping method by Ge et al. with the summarization levels of Cras et al. because Cras et al. shows the importance of clustering (grouping) data based on attributes into a hierarchy of levels and aggregating fact values at different levels of summarization, and a person of ordinary skill in the art would understand that visualizing data with the aid of levels of summarization would enable better visualization of the correlation of data, (Cras et al., paragraph 172-176). Therefore, one of ordinary skill in the art would recognize the claimed process as a combination of routine applications that are well known the art that and produce no more than expected results.

Claim 11 is rejected under 35 U.S.C. 103(a) as being unpatentable over Ge et al. (Nature Genetics, 2001, 29, 482-486) in view of Cras et al. (US 2002/0091681) as applied to claims 1-10, 12, 13, 15 and 16 above, and further in view of Artymiuk et al. (J. Mol. Biol., 1994, 243, 327-344).

The instant claim 11 depends from claim 1 with the extra limitation that wherein as the biological events, a structural unit is defined on the basis of atoms in a molecule or a set of atoms in a molecule for each molecule in a complex of one or more molecules, a representative position of the structural unit is defined on the basis of the

coordinates of atoms of which the structural unit is composed, and information about the distance between the representative positions of the structural units is displayed in the cells in the matrix, said matrix having each of the structural units as elements in the rows and columns thereof.

Ge et al. and Cras et al. are applied to claims 1-10, 12, 13, 15 and 16 above. Ge et al. and Cras et al. do not show a matrix with rows and columns of cells encompassing structural units of molecules, wherein the structural unit are atom(s) in a molecule, with information about distances between structural units.

Artymiuk et al. shows a matrix with rows and columns of cells encompassing structural units of a protein, wherein the structural units are the atoms of amino acids (Histidine 57, Serine 195 and Aspartate 102) encompassing a serine-protease catalytic triad, and providing distances between the respective structural units, (page 331; Figures 2-3).

It would have been obvious to one of ordinary skill in the art at the time of the instant invention to modify the transcriptome-interactome correlation mapping method by Ge et al. with the summarization levels of Cras et al. and the matrix of structural units with respective distances by Artymiuk et al. because Cras et al. shows the importance of clustering (grouping) data based on attributes into a hierarchy of levels and aggregating fact values at different levels of summarization, and a person of ordinary skill in the art would understand that visualizing data with the aid of levels of summarization and the aid of matrices with corresponding structural units would enable better visualization of the correlation of data, (Cras et al., paragraph 172-176; Artymiuk

et al. Figures 2-3 and 6). Therefore, one of ordinary skill in the art would recognize the claimed process as a combination of routine applications that are well known the art that and produce no more than expected results.

Response to Arguments

Applicant's arguments filed 05 December 2008 have been fully considered but they are not persuasive.

Applicant's argue that they are in the process of obtaining a verified English translation of Applicant's earlier foreign priority application (JP 2003-348438) filed 07 October 2003 that supports the instant claims and likewise antedates the filing date of US Pat. Pub. 2005/0010566 (Cushing).

Applicant's argument is not persuasive.

The current rejections under 35 U.S.C. 103(a) of claims 1-10, 12, 13 and 15 as being unpatentable over Ge et al. (Nature Genetics, 2001, 29, 482-486) in view of Cushing et al. (US 2005/0010566) and claim 11 being unpatentable over Ge et al. (Nature Genetics, 2001, 29, 482-486) in view of Cushing et al. (US 2005/0010566) as applied to claims 1-10, 12, 13 and 15 above, and further in view of Artymiuk et al. (J. Mol. Biol., 1994, 243, 327-344) will be maintained until a verified English translation of Applicant's foreign priority application (JP 2003-348438) is received and it is determined that the JP application supports all the instant claims.

Conclusion

No claims is allowed.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to LARRY D. RIGGS II whose telephone number is (571)270-3062. The examiner can normally be reached on Monday-Thursday, 7:30AM-5:00PM, ALT. Friday, EST.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Marjorie Moran can be reached on 571-272-0720. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free). If you would like assistance from a USPTO Customer Service Representative or access to the automated information system, call 800-786-9199 (IN USA OR CANADA) or 571-272-1000.

/ERIC S. DEJONG/
Primary Examiner, Art Unit 1631

/LDR/
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